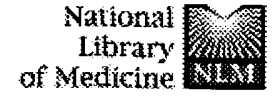

1: Jones AL, Hulett MD, Parish CR. Related Articles, Link

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PMID: 15138272 [PubMed - in process]

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PMID: 10747789 [PubMed - indexed for MEDLINE]

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IN El-Shabrawi Yosuf; Holley Kristine; Liu Dongfang; Pojasek Kevin; Sasisekharan Ram; Shriver Zachary; Venkataraman Ganesh
PA Unassigned Or Assigned To Individual (68000)
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PRAI US 2000-187846P 20000308 (Provisional)
FI US 2003099628 20030529
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
CLMN 60
GI 16 Figure(s).
FIG. 1 is a graph depicting the effect of DEPC inactivation of heparinase III on rate constant.
FIG. 2 is a graph depicting the pH dependence of the second order rate constant of inactivation upon incubation of heparinase III with varying concentrations of DEPC.
FIG. 3 is a graph depicting the quantification of DEPC-modified **histidine** residues in **heparinase III** over a period of time.
FIG. 4 is a graph depicting the substrate protection of heparinase III· inactivation by DEPC III.
FIG. 5 is a reverse phase HPLC profile of a lys-C digest of heparinase III which was not exposed to DEPC (top panel) and a peptide profile of heparinase III labeled with DEPC (bottom panel).
FIG. 6 is a series of graphs depicting SAX analysis of exhaustive heparinase III digests of heparan sulfate. Heparan sulfate was digested with either heparinase III from F. heparinum (panel A), recombinant heparinase III (panel B), H295A mutant enzyme (panel C), H510A mutant enzyme (panel D), or the H105A mutant enzyme (panel E).
FIG. 7 depicts a circular dichroism analysis of recombinant heparinase III and the H295A mutant enzyme, and the H510A mutant enzyme.
FIG. 8 is a graph depicting tumor volume in mice, as well as mice treated with heparinase I.
FIG. 9 is a bar graph depicting number of lung nodules that developed 13 days after tail vein injection of B16 BL6 cells. The cells were either

treated with PBS, heparinase I, or heparinase III.
FIG. 10, panel A, depicts the tumor volume of mice that were treated with GAG fragments generated from treatment of B16 BL6 cells with either heparinase I, heparinase III, or PBS or fragments generated from heparinase I treatment of LLC cells. Tumor volume was measured over time between 7 and 15 days postinjection of the tumor cells.
FIG. 10, panel B is a bar graph which quantitates the number of lung nodules of the mice described in panel A.
FIG. 11 is a bar graph depicting the effect on B16 cellular migration and invasion of transfection with antisense 2OST in pcDNA3.1.
FIG. 12 shows bar graphs depicting the ability of the transfected cells of FIG. 12 to develop into primary tumors as assessed by mean tumor volume (12a) and tumor weight (12b).
FIG. 13 depicts the results of compositional analysis of HLGAG saccharide fragments released from B16BL6 cells.
FIG. 14 is a bar graph depicting FGF2 signaling modulated by HLGAG fragments
FIG. 15 is a table (15a) and a schematic depicting the modulation of FGF2 activity in vivo by B16BL6 fragments (15b).

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IN El-Shabrawi Yosuf (AT); Holley Kristine; Liu Dongfang; Pojasek Kevin; Sasisekharan Ram; Shriver Zachary; Venkataraman Ganesh
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FI US 2002122793 20020905
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
CLMN 60
GI 16 Figure(s).
FIG. 1 is a graph depicting the effect of DEPC inactivation of heparinase III on rate constant.
FIG. 2 is a graph depicting the pH dependence of the second order rate constant of inactivation upon incubation of heparinase III with varying concentrations of DEPC.
FIG. 3 is a graph depicting the quantification of DEPC-modified **histidine** residues in **heparinase III** over a period of time.
FIG. 4 is a graph depicting the substrate protection of heparinase III inactivation by DEPC III.
FIG. 5 is a reverse phase HPLC profile of a lys-C digest of heparinase III which was not exposed to DEPC (top panel) and a peptide profile of heparinase III labeled with DEPC (bottom panel).
FIG. 6 is a series of graphs depicting SAX analysis of exhaustive heparinase III digests of heparan sulfate. Heparan sulfate was digested with either heparinase III from F. heparinum (panel A), recombinant heparinase III (panel B), H295A mutant enzyme (panel C), H510A mutant enzyme (panel D), or the H105A mutant enzyme (panel E).
FIG. 7 depicts a circular dichroism analysis of recombinant heparinase III and the H295A mutant enzyme, and the H510A mutant enzyme.
FIG. 8 is a graph depicting tumor volume in mice, as well as mice treated with heparinase I.
FIG. 9 is a bar graph depicting number of lung nodules that developed 13 days after tail vein injection of B16 BL6 cells. The cells were either treated with PBS, heparinase I, or heparinase III.

FIG. 10, panel A, depicts the tumor volume of mice that were treated with GAG fragments generated from treatment of B16 BL6 cells with either heparinase I, heparinase III, or PBS or fragments generated from heparinase I treatment of LLC cells. Tumor volume was measured over time between 7 and 15 days postinjection of the tumor cells.

FIG. 10, panel B is a bar graph which quantitates the number of lung nodules of the mice described in panel A.

FIG. 11 is a bar graph depicting the effect on B16 cellular migration and invasion of transfection with antisense 20ST in pcDNA3.1.

FIG. 12 shows bar graphs depicting the ability of the transfected cells of FIG. 12 to develop into primary tumors as assessed by mean tumor volume (12a) and tumor weight (12b).

FIG. 13 depicts the results of compositional analysis of HLGAG saccharide fragments released from B16BL6 cells.

FIG. 14 is a bar graph depicting FGF2 signaling modulated by HLGAG fragments

FIG. 15 is a table (15a) and a schematic depicting the modulation of FGF2 activity in vivo by B16BL6 fragments (15b).

L2 ANSWER 4 OF 6 DISSABS COPYRIGHT (C) 2004 ProQuest Information and Learning Company; All Rights Reserved on STN
AN 2002:39656 DISSABS Order Number: AAI0803378
TI Sequencing complex polysaccharides
AU Shriver, Zachary [Ph.D.]; Sasisekharan, Ram [adviser]
CS Massachusetts Institute of Technology (0753)
SO Dissertation Abstracts International, (2001) Vol. 63, No. 1B, p. 380. Order No.: AAI0803378.
DT Dissertation
FS DAI
LA English

L2 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 3
AN 2000:313840 BIOSIS
DN PREV200000313840
TI Histidine 295 and histidine 510 are crucial for the enzymatic degradation of heparan sulfate by heparinase III.
AU Pojasek, Kevin; Shriver, Zachary; Hu, Yini; Sasisekharan, Ram [Reprint author]
CS 16-561, MIT, Cambridge, MA, 02139, USA
SO Biochemistry, (April 11, 2000) Vol. 39, No. 14, pp. 4012-4019. print. CODEN: BICHAW. ISSN: 0006-2960.
DT Article
LA English
ED Entered STN: 26 Jul 2000
Last Updated on STN: 7 Jan 2002
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'BIB' IS NOT A VALID FORMAT
In a multifile environment, a format can only be used if it is valid
in at least one of the files. Refer to file specific help messages
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L2 ANSWER 6 OF 6 GENBANK® COPYRIGHT 2004 on STN

LOCUS (LOC): SCO939105 GenBank (R)
GenBank ACC. NO. (GBN): AL939105 AL109974 AL117385 AL117387 AL117669 AL121596 AL121600 AL121719 AL121849 AL121855 AL132662 AL132707 AL645882
GenBank VERSION (VER): AL939105.1 GI:24418991

CAS REGISTRY NO. (RN): 468711-59-3
SEQUENCE LENGTH (SQL): 291000
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Bacteria
DATE (DATE): 11 Feb 2003
DEFINITION (DEF): Streptomyces coelicolor A3(2) complete genome; segment 2/29.
SOURCE: Streptomyces coelicolor A3(2)
ORGANISM (ORGN): Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
NUCLEIC ACID COUNT (NA): 39089 a 105537 c 106715 g 39659 t
COMMENT:
On or before Oct 29, 2002 this sequence version replaced gi:20520891, gi:20520894, gi:20520895, gi:20520772, gi:20520896, gi:20520897, gi:20520883, gi:20520899, gi:20520902.
REFERENCE: 1
AUTHOR (AU): Bentley,S.D.; Chater,K.F.; Cerdeno-Tarraga,A.M.; Challis,G.L.; Thomson,N.R.; James,K.D.; Harris,D.E.; Quail,M.A.; Kieser,H.; Harper,D.; Bateman,A.; Brown,S.; Chandra,G.; Chen,C.W.; Collins,M.; Cronin,A.; Fraser,A.; Goble,A.; Hidalgo,J.; Hornsby,T.; Howarth,S.; Huang,C.H.; Kieser,T.; Larke,L.; Murphy,L.; Oliver,K.; O'Neil,S.; Rabbinowitsch,E.; Rajandream,M.A.; Rutherford,K.; Rutter,S.; Seeger,K.; Saunders,D.; Sharp,S.; Squares,R.; Squares,S.; Taylor,K.; Warren,T.; Wietzorrek,A.; Woodward,J.; Barrell,B.G.; Parkhill,J.; Hopwood,D.A.
TITLE (TI): Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)
JOURNAL (SO): Nature, 417 (6885), 141-147 (2002)
OTHER SOURCE (OS): CA 136:396750
REFERENCE: 2 (bases 1 to 291000)
AUTHOR (AU): Bentley,S.D.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: sdb@sanger.ac.uk

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..291000	/organism="Streptomyces coelicolor A3(2)" /strain="A3(2)" /db-xref="taxon:100226"
gene	213..3092	/gene="SCO0305" /note="synonym: SC5G9.14"
CDS	213..3092	/gene="SCO0305" /note="SC5G9.14, hypothetical protein, len: 959 aa; unknown function, similar to TR:O54182 (EMBL:AL021411) Streptomyces coelicolor hypothetical protein (913 aa), fasta scores; opt: 698 z-score: 776.6 E(): 0, 27.0% identity in 972 aa overlap. The C-terminus shows very weak similarity to eukaryotic beta-transducins e.g. SW:GBB4-MOUSE (EMBL:S86124), gnb4,

```
                                     Mus musculus guanine
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                                     subunit 4 (340 aa) (23.0% identity
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                                         /note="SC5G9.15c, possible
                                         pseudogene, len: 302 aa; similar
                                         to hypothetical proteins e.g.
                                         SW:YCJY-ECOLI (EMBL:AE000230),
                                         YcjY, Escherichia coli
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                                         frameplot and codon usage plots
                                         indicate a coding region which
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                                probable CDS suggested by GC
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                                preference. Similar to possible
                                DNA-binding proteins from S.
                                coelicolor e.g. SCJ9A.15c (cosmid
                                SCJ9A), S. coelicolor possible
                                DNA-binding protein (290 aa)
                                (39.3% identity in 298 aa
                                overlap). Contains probable
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                                35-56 (Score 1197, +3.26 SD)"
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                                PQLRRLLDDLTHTPALVLGRCTDILAWNPPAAAL
                                FTDFALLSRDERNFVRLVFRDPAV
                                RALYTDWPYMARACVAQLRMEAARDPHDPRLSAL
                                VAELSAQDPDFRTWWKDHRVAVRG
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                                protein, len: 467 aa; unknown
                                function, probable CDS suggested
                                by GC frameplot, positional base
                                preference and amino acid
                                composition. Contains hydrophobic,
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                                (leucine) codon; possible target
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                                GDSDTIAETLYATWQDRSAIRVGGVPLTAWLDER
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                                LDSGTGATLGIRRPETLNNAGQTM
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                                                possible target for bldA
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CDS             complement(6537..7625)          /gene="SCO0309"
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                                                hydrolase, len: 362 aa; similar to
                                                6-aminohexanoate-dimer hydrolases
                                                which degrade
                                                N-(6-aminohexanoyl)-6-aminohexanoa
                                                te e.g. TR:P75007 (EMBL:K02336),
                                                NylB', Flavobacterium sp. (strain
                                                K172) 6-aminohexanoic acid linear
                                                oligomer hydrolase (EII') (392
                                                aa), fasta scores; opt: 531
                                                z-score: 598.0 E(): 6.1e-26, 34.1%
                                                identity in 323 aa overlap"
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CDS             complement(7816..8466)          /gene="SCO0310"
                                                /note="SC5G9.19c, possible
                                                tetR-family transcriptional
                                                regulator, len: 141 aa; shows
                                                similarity to the N-terminal half
                                                of TR:O24741 (EMBL:AB001683),
                                                FarA, Streptomyces sp. strain
                                                FRI-5 receptor for an
                                                extracellular regulatory factor
                                                (IM-2) (221 aa), fasta scores;
                                                opt: 154 z-score: 193.4 E():
                                                0.0021, 36.7% identity in 79 aa
                                                overlap and to putative
                                                transcriptional regulators:
                                                Contains Pfam match to entry
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PF00440 tetR, Bacterial regulatory proteins, tetR family"
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GVYQVILRGEGDGRALREFTELIRSHAEMAFRDR
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misc-feature complement(8278..8418)
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/note="Pfam match to entry PF00440 tetR, Bacterial regulatory proteins, tetR family, score 31.50, E-value 5.4e-07"

gene 8575..10131
/gene="SCO0311"
/note="synonym: SC5G9.20"

CDS 8575..10131
/gene="SCO0311"
/note="SC5G9.20, probable ligase, len: 518 aa; similar to domains within polyketide synthases e.g. to the N-terminus of TR:Q54297 (EMBL:X86780), RapA, Streptomyces hygroscopicus polyketide synthase (8563 aa), fasta scores; opt: 815 z-score: 894.4 E(): 0, 34.0% identity in 509 aa overlap and to SW:DHBE-BACSU (EMBL:U26444), DhbE, EntE, Bacillus subtilis 2,3-dihydroxybenzoate-AMP ligase (539 aa) (31.3% identity in 520 aa overlap). Also similar to others from S. coelicolor e.g. TR:Q9Z5A6 (EMBL:AL035478) S. coelicolor probable long-chain-fatty-acid-CoA ligase (541 aa) (35.9% identity in 537 aa overlap). Contains Pfam match to entry PF00501 AMP-binding, AMP-binding enzyme and PS00455 Putative AMP-binding domain signature"
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CDS             10147..11316         /gene="SCO0312"
                                     /note="SC5G9.21, probable acyl-CoA
                                     dehydrogenase, len: 389 aa;
                                     similar to both bacterial and
                                     eukaryotic acyl-CoA dehydrogenases
                                     e.g. SW:ACDS-HUMAN (EMBL:M26393),
                                     AcaDS, Homo sapiens mitochondrial
                                     acyl-CoA dehydrogenase short-chain
                                     specific precursor (412 aa), fasta
                                     scores; opt: 653 z-score: 771.4
                                     E(): 0, 34.8% identity in 376 aa
                                     overlap. Also similar to
                                     SCI30A.22C (EMBL:AL096811)
                                     Streptomyces coelicolor probable
                                     acyl-CoA dehydrogenase. Contains 2
                                     Pfam matches to entry PF00441
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```
                                     dehydrogenase, score 155.40,
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RBS             11367..11371         /note="possible RBS"
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                                     /note="synonym: SC5G9.22"
CDS             11378..12727         /gene="SCO0313"
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                                     transmembrane transport protein,
                                     len: 449 aa; similar to many
                                     transmembrane transporters e.g.
                                     SW:DGOT-ECOLI (EMBL:L10328), dgoT,
                                     Escherichia coli D-galactonate
                                     transporter (445 aa), fasta
                                     scores; opt: 332 z-score: 376.2
                                     E(): 1.4e-13, 23.7% identity in
                                     438 aa overlap. Contains
                                     hydrophobic, possible
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                                     Contains Pfam match to entry
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misc-feature    11462..12700         /gene="SCO0313"
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CDS             12724..14670         /gene="SCO0314"
                                     /note="SC5G9.23, putative secreted
                                     protein, len: 648 aa; unknown
                                     function, similar to TR:Q52556
                                     (EMBL:M86744), SdsA, Pseudomonas
                                     sp. alkyl sulfatase which degrades
                                     sulfate esters of long-chain
                                     primary alcohols (SDS) (528 aa),
                                     fasta scores; opt: 739 z-score:
                                     806.7 E(): 0, 29.7% identity in
                                     528 aa overlap, but having an
                                     N-terminal extension of approx.
                                     140 aa. Similar to TR:Q48790
```

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                                        (EMBL:X92423), SepA, Listeria
                                        monocytogenes gene implicated in
                                        cell separation (391 aa) (42.6%
                                        identity in 364 aa overlap). Also
                                        similar to hypothetical proteins
                                        e.g. TR:O69728 (EMBL:AL022121)
                                        Mycobacterium tuberculosis
                                        hypothetical protein (626 aa)
                                        (52.9% identity in 624 aa
                                        overlap). Contains Pfam match to
                                        entry PF00753 lactamase-B,
                                        Metallo-beta-lactamase
                                        superfamily. Contains possible
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                                        LDWHIGDTYWHLRLANGVLTWTSDASPDPDAGLT
                                        MTMTRAQLLAVLAGKGTDGVTMTG
                                        DGTQLVRLLSVLDTADHRFPVVTP"
misc-feature    13090..13773            /gene="SCO0314"
                                        /note="Pfam match to entry PF00753
                                        lactamase-B,
                                        Metallo-beta-lactamase
                                        superfamily, score 69.40, E-value
                                        7.3e-17"
gene            complement(14697..16055 /gene="SCO0315"
                )
                                        /note="synonym: SC5G9.24c"
CDS             complement(14697..16055 /gene="SCO0315"
                )
                                        /note="SC5G9.24c, probable
                                        decarboxylase, len: 452 aa;
                                        similar to many e.g. SW:DCDA-BACSU
                                        (EMBL:L09228), LysA, Bacillus
                                        subtilis diaminopimelate
                                        decarboxylase (441 aa), fasta
                                        scores; opt: 484 z-score: 542.1
                                        E(): 7.9e-23, 31.6% identity in
```

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                                     389 aa overlap. Similar to
                                     TR:Q9ZBH5 (EMBL:AL035206), DcdA,
                                     Streptomyces coelicolor
                                     diaminopimelate decarboxylase (440
                                     aa), fasta scores; opt: 400
                                     z-score: 384.5 E(): 3.6e-16, 30.2%
                                     identity in 427 aa overlap.
                                     Contains 2 Pfam matches to entry
                                     PF00278 Orn-DAP-Arg-deC,
                                     Pyridoxal-dependent decarboxylase,
                                     PS00879 Orn/DAP/Arg decarboxylases
                                     family 2 signature 2 and PS00878
                                     Orn/DAP/Arg decarboxylases family
                                     2 pyridoxal-P attachment site"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative decarboxylase"
                                     /protein-id="CAB55672.1"
                                     /db-xref="GI:5881872"
                                     /translation="MTSGSLHQRGTAREAALARA
                                     VEDGLLGPRTPLVGLLDVDGVLAA
                                     VDALNEAFEGPAPVQHTFAAKACGLVPVLRLLAE
                                     AGMGCEVASPGELEQALAAGFTYD
                                     RLVFDSPAKTVEELEFALAHGIAINLDNFQEMAR
                                     VDGLLAGREAAGPIGLRVNPQVGA
                                     GAIGAMSTATATSKFGVALRDEGAVDAVIEAFAR
                                     RPWLNRLHAHVGSQGCPLPLIAQG
                                     VRTAYELAERINRELGRAQITGLDIGGGLPVNFD
                                     GEDDRPTYADHVAELRSAAPGLFD
                                     GRYALITEFGRSLLAKSGTIASVVEYTKSAGGRR
                                     IAVTHAGAQVATRTVFMPDAWPLR
                                     VGVFDAAGRPKQGPAEVVDIAGPCCFAGDLTATG
                                     RELPAVEPGDVVALYDTGAYYFSS
                                     HFSYNSLPRPAVYGYRTDSRGQIAFALVREAQSV
                                     RAVVEESGLAQADALVALGTDQSA ER"
misc-feature    complement(14859..15020
                )                    /gene="SCO0315"

                                     /note="Pfam match to entry PF00278
                                     Orn-DAP-Arg-deC,
                                     Pyridoxal-dependent decarboxylase,
                                     score 28.10, E-value 1.2e-07"
misc-feature    complement(15105..15905
                )                    /gene="SCO0315"

                                     /note="Pfam match to entry PF00278
                                     Orn-DAP-Arg-deC,
                                     Pyridoxal-dependent decarboxylase,
                                     score 135.90, E-value 7.7e-40"
misc-feature    complement(15312..15356
                )                    /gene="SCO0315"

                                     /note="PS00879 Orn/DAP/Arg
                                     decarboxylases family 2 signature
                                     2"
misc-feature    complement(15816..15872
                )                    /gene="SCO0315"

                                     /note="PS00878 Orn/DAP/Arg
                                     decarboxylases family 2
                                     pyridoxal-P attachment site"
gene            complement(16254..17921
                )                    /gene="SCO0316"

                                     /note="synonym: SC5G9.25c"
CDS             complement(16254..17921
                )                    /gene="SCO0316"

                                     /note="SC5G9.25c, hypothetical
```

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                                     protein, len: 555 aa; similar to
                                     hypothetical proteins e.g.
                                     TR:O50442 (EMBL:AL010186)
                                     Mycobacterium tuberculosis
                                     hypothetical protein (538 aa),
                                     fasta scores; opt: 485 z-score:
                                     521.2 E(): 1.2e-21, 32.6% identity
                                     in 568 aa overlap and to TR:Q9Z561
                                     (EMBL:AL035569) S.coelicolor
                                     putative transcriptional regulator
                                     (415 aa) (28.4% identity in 444 aa
                                     overlap). Contains probable
                                     helix-turn-helix motif at aa
                                     505-526 (Score 1081, +2.87 SD)"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative DNA-binding
                                     protein"
                                     /protein-id="CAB55673.1"
                                     /db-xref="GI:5881873"
                                     /translation="MAAREPDRRDGRPSLEQILR
                                     LIAPGMLDVVVAPRGTGVPVADAV
                                     LHDPGEERDDGTWAASGLILLAVGVDAAAPEAID
                                     VLRGAERAGAAAVVLRRGARGPRA
                                     ALLEAAASGRTALLTRRPGQGWTEVLGQLRTALA
                                     HSAPTGGTGVEGLRLGDLPELANT
                                     VAALVGGAITIEDPQSRVLAYSRMDHEPDPMRRL
                                     TILGQEVPRWRVDELRESGFFQAL
                                     WNTDGVVRLPADDRYAERLAVAVRHGSEILGSLW
                                     AAADGRPLAEDAAAALHTAARAAV
                                     PHLAHHQTWGRAAARARESAVHALLDGSGPAARV
                                     AHDAGVAPDRPYTVLVAEAYDSRD
                                     LTAVPAPATGGAAGQRTLDVLALQAEAYRPGCVT
                                     ARSGRRLYVLIPAEDGETDPARAL
                                     TATARSVPRGVVFAGVGPVAADLSGLPASREAAE
                                     LVVRVLRERAARRPAADVVSAVAA
                                     FGEVVPEVSALRVLDLIAPLWQSLSGPVHAMVEH
                                     DRAHGSEYGASVGAYLDAFGDTGT
                                     AAQRLNVHPNTLRYRLRRARELFGVDLADPTLRL
                                     LADVGLRLARRTE"
gene        complement(17975..19237  /gene="SCO0317"
            )
                                     /note="synonym: SC5G9.26c"
CDS         complement(17975..19237  /gene="SCO0317"
            )
                                     /note="SC5G9.26c, probable
                                     transmembrane transport protein,
                                     len: 420 aa; shows weak similarity
                                     to many efflux pumps e.g.
                                     SW:CMLR-STRLI (EMBL:X59968), cmlR,
                                     Streptomyces lividans
                                     chloramphenicol resistance protein
                                     (392 aa), fasta scores; opt: 276
                                     z-score: 292.9 E(): 6e-09, 27.3%
                                     identity in 407 aa overlap.
                                     Contains hydrophobic, possible
                                     membrane-spanning regions"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative transmembrane
                                     transport protein"
                                     /protein-id="CAB55674.1"
                                     /db-xref="GI:5881874"
```

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                                     /translation="MSERATESVLRSPGIPHLLT
                                     VGAFCFAGLALLLPVSPAWAVAGG
                                     ADEFGAGLVTAVLMAATVLAQLCVRTALRTIGWP
                                     RTLALGALLLGLPALVQSLSDHLV
                                     PILVTTALRGAGFGIVTVCGATAAAALAPRGRQG
                                     AAIGLYGLAVALPQVILTPAAPWL
                                     MGTFALPAIVACGVLPVLALPWTRALGRAVEART
                                     DGPPTQDGRTGHPAPAATVLRRIL
                                     LPLTVLLLVTAAGGAVLTFAPQFTSTPALAATGL
                                     LALTATAALARWGCGELADRIALR
                                     PITALLASTACAGLALIALAVGPDGETVLPLLAG
                                     LLLLGTAYGGLQSLTLVQAFDLAG
                                     AEDRHMTSVAWNIGYDAGTGLGSLALGLAAQAAT
                                     FSAGFAVMSAVMAAVVLAVLLTPG
                                     RPAGRTAGDRPRTRSRTRRSPARPRKLP"
gene                 complement(19329..20345
                     )               /gene="SCO0318"

                                     /note="synonym: SC5G9.27c"
CDS                  complement(19329..20345
                     )               /gene="SCO0318"

                                     /note="SC5G9.27c, possible
                                     oxidoreductase, len: 388 aa; shows
                                     weak similarity to many eukaryotic
                                     and bacterial oxidoreductases e.g.
                                     TR:Q39617 (EMBL:U36752), LpcR-1,
                                     Chlamydomonas reinhardtii
                                     NADPH:protochlorophyllide
                                     oxidoreductase (397 aa), fasta
                                     scores; opt: 278 z-score: 296.3
                                     E(): 3.8e-09, 27.4% identity in
                                     343 aa overlap. Similar to
                                     TR:O53726 (EMBL:AL021932)
                                     Mycobacterium tuberculosis
                                     putative oxidoreductase (311 aa)
                                     (41.1% identity in 309 aa
                                     overlap). Similar to others from
                                     S. coelicolor e.g. SCJ9A.19c
                                     (cosmid SCJ9A), possible
                                     oxidoreductase (311 aa) (39.6%
                                     identity in 303 aa overlap).
                                     Contains Pfam match to entry
                                     PF00106 adh-short, short chain
                                     dehydrogenase"
                                     /codon-start=1
                                     /transl-table=11
                                     /product="putative oxidoreductase"
                                     /protein-id="CAB55675.1"
                                     /db-xref="GI:5881875"
                                     /translation="MGESVLLTSTPPEHKESVIV
                                     SSAPQSRPWDVHRLPSAEGRNFLV
                                     TGGNAGIGYFTAEQLAATGALVVIGSRNPAKADA
                                     ALASIRSRVPGARVRHLHLDLADL
                                     STLKSAVDGLALDLGRLDAVVHNAGGALDDPPRR
                                     ETEDGHELMFGTNHLGHYALTRWL
                                     APLLSAAPAGRVVTVGSFAARSERLDLDDLQSTR
                                     DYRPKRTYGRSKLAQMCFGFELDR
                                     RLRAAGSTVLSAVAHPGGALDSLTPPRPPVGAPT
                                     PGERLRGLPAALMVQGKDAGAWPV
                                     VRAVLDSDVQGGQLWGPRVFGLRGQPRREPVPAH
                                     MADPAVAARLWAASAELTGTTDPH LGFR"
misc-feature         complement(19626..20228
                     )               /gene="SCO0318"

                                     /note="Pfam match to entry PF00106
```

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                                    adh-short, short chain
                                    dehydrogenase, score 70.30,
                                    E-value 4e-17"
gene            complement(20499..21008 /gene="SCO0319"
                )
                                    /note="synonym: SC5G9.28c"
CDS             complement(20499..21008 /gene="SCO0319"
                )
                                    /note="SC5G9.28c, unknown, len:
                                    169 aa; probable CDS suggested by
                                    GC frameplot, positional base
                                    preference and amino acid
                                    composition"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="hypothetical protein
                                    SC5G9.28c"
                                    /protein-id="CAB55676.1"
                                    /db-xref="GI:5881876"
                                    /translation="MEAESGHAVVHQCGGRHRGQ
                                    PSGNRHDLLRTRDDLFGVSGPGSH
                                    DHTPADPARVHSVTDCQHLARPAATRHVRQRARE
                                    EVLTPAAAQQRVQEDDVGRDHTDD
                                    DLAGAGHGIGQVDQAQHVRSTERGHVDRMHEQHP
                                    SLEATSRPASNLKSGRGQGSSVVR
                                    GGVGPVGKG"
gene            21110..21583        /gene="SCO0320"
                                    /note="synonym: SC5G9.29"
CDS             21110..21583        /gene="SCO0320"
                                    /note="SC5G9.29, hypothetical
                                    protein, len: 157 aa; similar to
                                    the C-terminal half of
                                    SW:QOR-PSEAE (EMBL:X85015), qor,
                                    Pseudomonas aeruginosa quinone
                                    oxidoreductase (325 aa), fasta
                                    scores; opt: 223 z-score: 254.4
                                    E(): 8.3e-07, 34.8% identity in
                                    161 aa overlap and the
                                    corresponding region of many
                                    similar hypothetical proteins.
                                    Also similar to regions of
                                    polyketide synthase-type proteins
                                    e.g. SW:MCAS-MYCBO (EMBL:M95808),
                                    mas, Mycobacterium bovis
                                    mycocerosic acid synthase (2110
                                    aa) (35.8% identity in 159 aa
                                    overlap). Contains PS00017
                                    ATP/GTP-binding site motif A
                                    (P-loop)"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="hypothetical protein"
                                    /protein-id="CAB55677.1"
                                    /db-xref="GI:5881877"
                                    /translation="MVAAASSDAKLALARDLGAE
                                    VVVDYTRADWVERVREATGGGAAL
                                    VYDGAGGALGATSVDALADGGRFVTYGTADGFAA
                                    PDRESAARRGIRLLMPLMDGPPDQ
                                    ETARELLGLALESAAEGRLRPAIGATYPLARAAD
                                    AHRALAARTTVGKSLLLMGGE"
misc-feature    21536..21559        /gene="SCO0320"
                                    /note="PS00017 ATP/GTP-binding
                                    site motif A (P-loop)"
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gene            21699..23255        /gene="SCO0321"
                                    /note="synonym: SC5G9.30"
CDS             21699..23255        /gene="SCO0321"
                                    /note="SC5G9.30, probable
                                    carboxylesterase, len: 518 aa;
                                    similar to many eukaryotic and
                                    bacterial e.g. SW:PNBA-BACSU
                                    (EMBL:U06089), PrnbA, Bacillus
                                    subtilis 4-nitrobenzyl esterase
                                    (489 aa), fasta scores; opt: 718
                                    z-score: 774.9 E(): 0, 36.3%
                                    identity in 479 aa overlap.
                                    Similar to TR:Q9Z545
                                    (EMBL:AL035212) Streptomyces
                                    coelicolor probable
                                    carboxylesterase (502 aa) (41.3%
                                    identity in 521 aa overlap).
                                    Contains 2 Pfam matches to entry
                                    PF00135 COesterase,
                                    Carboxylesterases and PS00122
                                    Carboxylesterases type-B serine
                                    active site"
                                    /codon-start=1
                                    /transl-table=11
                                    /product="putative
                                    carboxylesterase"
                                    /protein-id="CAB55678.1"
                                    /db-xref="GI:5881878"
                                    /translation="MQREAVPVVVFKTRHGSVRG
                                    FRASGDVVAVLGVPYAAAPFGVHR
                                    FREPAPAPAWTGVRDGRSFGPVAPQSARLPGAPV
                                    WSPGDEDILTVNLWTPAPDGGPLP
                                    VLVWIHGGAYTFGSSAQPDFDGTVLARAGLVVVT
                                    LNYRIGFEGFGHVPPDGPIAHPDN
                                    RGLLDQVAALRWVRENIAAFGGEPGNVTVAGQSS
                                    GAASVACLMVMDRARGLFHRAIAH
                                    SPASPCYPRDIAAATTREVAAAAGCPATSAGLRS
                                    TTPQALVAAADQVADGYRRDPASG
                                    SRHYDPSLYAPVLDDDVLPTDPLTGMAAGAARDV
                                    DLLVCHTTEEYWLLDAVGSSAKVT
                                    TDAQLARFAEDFGLPDGLVAGYRAALPRAPVLDV
                                    YLAVFGDLLFGEYANRLAEVHARA
                                    GGRAFLSRFDRRRADPGAVVRAWHCADVPFAFGN
                                    LDDERLAFLIGGAPTAADQGLARR
                                    MVRAWADFAATGSPGWPPVRDSSTEATEATEATE
                                    AKVWTADPHAARTGDRAAAVRALW
                                    AEADFPVLRP"
misc-feature    21735..22658        /gene="SCO0321"
                                    /note="Pfam match to entry PF00135
                                    COesterase, Carboxylesterases,
                                    score 250.70, E-value 2.9e-72"
misc-feature    22236..22283        /gene="SCO0321"
                                    /note="PS00122 Carboxylesterases
                                    type-B serine active site"
misc-feature    22944..23186        /gene="SCO0321"
                                    /note="Pfam match to entry PF00135
                                    COesterase, Carboxylesterases,
                                    score 12.90, E-value 0.0041"
gene            complement(23244..24938
                )                   /gene="SCO0322"
                                    /note="synonyms: SC5G9.31c,
                                    SCF12.01c"
CDS             complement(23244..24938 /gene="SCO0322"
```

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                )
                                        /note="SCF12.01c, possible ABC
                                        transport ATP-binding subunit,
                                        len: >230aa; similar to many eg.
                                        SW:TLRC-STRFR tylosin resistance
                                        ATP-binding protein from
                                        Streptomyces fradiae (548 aa)
                                        fasta scores; opt: 1017, z-score:
                                        1131.8, E(): 0, (69.0% identity in
                                        232 aa overlap). Contains Prosite
                                        match to PS00211 ABC transporters
                                        family signature and Prosite match
                                        to PS00017 ATP/GTP-binding site
                                        motif A (P-loop). SC5G9.31c,
                                        probable ABC-transporter
                                        ATP-binding protein, partial CDS,
                                        len: >371 aa; similar ATP-binding
                                        components from antibiotic
                                        resistance export systems e.g.
                                        SW:TLRC-STRFR (EMBL:M57437), tlrC,
                                        Streptomyces fradiae tylosin
                                        resistance ATP-binding protein
                                        (548 aa), fasta scores; opt: 1517
                                        z-score: 1597.3 E(): 0, 67.4%
                                        identity in 356 aa overlap. Also
                                        similar to many other putative
                                        ABC-transporter ATP-binding
                                        proteins. Contains Pfam match to
                                        entry PF00005 ABC-tran, ABC
                                        transporter, PS00211 ABC
                                        transporters family signature and
                                        PS00017 ATP/GTP-binding site motif
                                        A (P-loop)"
                                        /codon-start=1
                                        /transl-table=11
                                        /product="putative ABC transport
                                        ATP-binding subunit"
                                        /protein-id="CAD55436.1"
                                        /db-xref="GI:24418992"
                                        /translation="MRTSQLTLSHVTKRYAGRTV
                                        LDQVSLTLKPGEKAGLIGDNGAGK
                                        STLLRIVAGQERPDSGEATVTAAGGIGCLPQSVP
                                        LPPTATVQDAVDLSLADLRALEAE
                                        LRRAEQALGAGEDPEALAAYTVLVERYEARDGHD
                                        ADRRVDIALHHLGLPALRRERRLG
                                        TLSGGERSRLALAGVLAGRPEVLLLDEPTNDLDD
                                        QAVEWLETQLRAHRGTVLAVTHDR
                                        VFLERLTSTILEAEGGRVTRYGDGYNGYRTAKAA
                                        ERRRRLQEHEEWRSELARNERLAT
                                        GHAARLGAIPRKASLANFGHGGFRARGRAHGAMS
                                        RIRNARERVERLTENPVAPPPDAL
                                        AFTVRMATAAEEASATGAASATLPAVQLSDVRVG
                                        DRLHLGSLGLGRRGRLLVTGPNGA
                                        GKTTLLKVLAGELRPDEGSVRVPGRVGHLRQEET
                                        PWPPELTVAEAFGLGRVGAADEHA
                                        DTLLALGLFRPAELRLRMGELSYGQRRRVELARL
                                        VSEPVDLLLLDEPTNHLSPALVEE
                                        LEEALTGFSGAIVLVTHDRALRGRFRGRRLTLPA
                                        APGARTGQPVAVAHRPRPGSGA"
misc-feature    complement(23310..23798 /gene="SCO0322"
                )
                                        /note="Pfam match to entry PF00005
                                        ABC-tran, ABC transporter, score
```

144.30, E-value 2.1e-39"